

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2001, 18:15:30 ; Search time 11120.8 Seconds
(without alignments)
3070.050 Million cell updates/sec

Title: US-09-284-180-4

Perfect score: 2315
Sequence: 1 ggggggtgcctctatgctgc.....cgttaataacatagtgcttc 2315

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1283235 segs, 737329652 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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95: gb_v48:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2258	97.5	2893	9 AX003081
2	2250	97.2	2672	85 AB021292
3	2156	93.1	2894	9 AX003083
4	1978	85.4	2400	85 AB022317
5	1726	74.6	1913	88 AF053369
6	1164	50.3	126228	86 AC006543
7	1164	50.3	171964	81 AL451003
8	1164	50.3	172010	70 AC026541
9	1164	50.3	234523	86 AC006544
10	1043	45.1	163903	86 AC007387
11	623	26.9	799	9 AX003085

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14	211	9.1	413	54	G22417	human STS W
15	159	6.9	2669	85	AB047604	Macaca fa
16	157	6.8	1581	88	AF119878	Macaca fa
17	75	3.2	4008	94	AB002563	Macaca fa
18	45	1.9	4002	94	AB002563	Rattus no
19	39	1.7	3205	94	AB022311	Mus muscu
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ALIGNMENTS

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LOCUS      Sequence 1 from Patent EP0933425.
DEFINITION  AX003081
ACCESSION  AX003081
VERSION    AX003081.1  GI:9926964
KEYWORDS
SOURCE     human.
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 2893)
AUTHORS    Michalovich, D. and Doe, T.R.
TITLE       Semaphorin family polypeptides and polynucleotides
JOURNAL     Patent: EP 0933425-A 1 04-AUG-1999;
           SMITHKLINE BEECHAM PLC (GB)
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Query Match 97.5%; Score 2258; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
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JOURNAL	Encinas,J.A., Kikuchi,K., Chedotal,A., de Castro,F., Goodman,C.S.		
MEDLINE	and Kimura,T.		
REFERENCE	Cloning, expression, and genetic mapping of Sema W, a member of the		
AUTHORS	semaphorin family		
TITLE	Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2491-2496 (1999)		
JOURNAL	99162633		
	2 (bases 1 to 2672)		
	Encinas,J.A., Ishida,H. and Kimura,T.		
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	Kimura, Sumitomo Pharmaceuticals Research Center, 3-1-98		
	Kasugade-naka, Konohana, Osaka 554-0022, Japan		
	(E-mail:t.kimura@sumitomopharm.co.jp, Tel:81-6-6466-5228,		
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DB	492	GCCCAAGCCTTTGTGTGCGACGCCGTGGCCTTGAGACCACCGAATGGGGATGAAATGGA	551
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VERSION AX003083.1 GI:9926965
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SOURCE human.

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REFERENCE	1 (bases 1 to 2894)
AUTHORS	Michalovich, D. and Doe, T. R.
TITLE	Semaphorin family polypeptides and polynucleotides
JOURNAL	Patent: EP 0933425-A 3 04-NUG-1999;
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 SOURCE Homo sapiens adult brain, hippocampus cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Encinas,J.A., Kikuchi,K., Chedotal,A., de Castro,F., Goodman,C.S.
 and Kimura,T.
 TITLE Cloning, expression, and genetic mapping of Sema W, a member of the
 semaphorin family
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2491-2496 (1999)
 MEDLINE 99162633
 REFERENCE 2 (bases 1 to 2400)
 AUTHORS Jeffrey,E.A., Ishida,H. and Kimura,T.
 TITLE Direct Submission
 JOURNAL Submitted (11-JAN-1999) to the DDBJ/EMBL/GenBank databases. Toru
 Kimura, Sumitomo Pharmaceuticals Co. Ltd., Research Center, 3-1-98,
 Kaugade-naka, Konohana, Osaka 554-0022, Japan
 (E-mail:tkimura@sumitomopharm.co.jp, Tel:81-6-466-5228,
 Fax:81-6-466-5491)
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 DEFINITION Homo sapiens chromosome 2p13 clone bac172k1, complete sequence.
 AC006543.7 GI:4388738
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 KEYWORDS
 SOURCE
 ORGANISM
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 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
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 Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.
 Homo sapiens Chromosome 2p13 BAC Clone bac172k1
 Unpublished
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 2 (bases 1 to 126228)
 Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.
 Direct Submission
 Submitted (09-FEB-1999) Department of Chemistry and Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 3 (bases 1 to 126228)
 Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.
 Direct Submission
 Submitted (09-MAR-1999) Department of Chemistry and Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 4 (bases 1 to 126228)
 Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.
 Direct Submission


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coverage: 4.10x in Q20 bases; agarose-1p
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Draft Sequence Produced by Whitehead Institute/MIT Center for
Genome Research, 320 Charles Street,
Cambridge, MA 02141, USA
http://www-seq.wi.mit.edu.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 3477: contig of 3477 bp in length
* 3478 3577: gap of 100 bp
* 3578 13586: contig of 10009 bp in length
* 13587 13686: gap of 100 bp
* 13687 18688: contig of 5002 bp in length
* 18689 18788: gap of 100 bp
* 18789 26165: contig of 7377 bp in length
* 26166 26265: gap of 100 bp
* 26266 52879: contig of 26614 bp in length
* 52880 52979: gap of 100 bp
* 52980 82107: contig of 29128 bp in length
* 82108 82207: gap of 100 bp
* 82208 88054: contig of 5847 bp in length
* 88055 88154: gap of 100 bp
* 88155 91774: contig of 3620 bp in length
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* 91875 101902: contig of 10028 bp in length
* 101903 102002: gap of 100 bp
* 102003 109337: contig of 7335 bp in length
* 109338 109437: gap of 100 bp
* 109438 113399: contig of 3962 bp in length
* 113400 113499: gap of 100 bp
* 113500 118719: contig of 5220 bp in length
* 118720 118819: gap of 100 bp
* 118820 123815: contig of 4996 bp in length
* 123816 123915: gap of 100 bp
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* 132493 132592: gap of 100 bp
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* 137710 137809: gap of 100 bp
* 137810 149420: contig of 11611 bp in length
* 149421 149520: gap of 100 bp
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*	116576	116675:	gap of 100 bp	
*	116676	128108:	contig of 11433 bp in length	
*	128109	128308:	gap of 100 bp	
*	128209	140666:	contig of 12460 bp in length	
*	140669	140768:	gap of 100 bp	
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DEFINITION	Homo sapiens chromosome 2p13 clone bac91a19, complete sequence.		
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VERSION	AC006544.19	GI:4630756	
KEYWORDS	HTG.		
SOURCE	human.		
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AUTHORS	1 (bases 1 to 234523)		
TITLE	Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 234523)		
AUTHORS	Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-FEB-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA		
REFERENCE	3 (bases 1 to 234523)		
AUTHORS	Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-APR-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA		
REFERENCE	4 (bases 1 to 234523)		
AUTHORS	Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-APR-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA		
REFERENCE	5 (bases 1 to 234523)		
AUTHORS	Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-MAY-2000) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA		
REFERENCE	6 (bases 1 to 234523)		
AUTHORS	Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-MAY-2000) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA		
REFERENCE	7 (bases 1 to 234523)		
AUTHORS	Chen, F., Do, A., Do, T., Weisler, M. and Roe, B. A.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-MAY-2000) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA		
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VERSION AC007387.3 GI:5931456
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
99063792
MEDLINE
REFERENCE
AUTHORS Cordes, M., Stromolt, C., Mauph, R., Yoakum, M. and Le, T.
TITLE The sequence of Homo sapiens BAC clone RP11-372J12
JOURNAL Unpublished.
REFERENCE
AUTHORS Waterston, R.H.
TITLE 3 (bases 1 to 163903)
JOURNAL Direct Submission
Submitted (25-APR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 163903)
JOURNAL Waterston, R.H.
TITLE Direct Submission
Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 163903)
JOURNAL Waterston, R.
TITLE Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 28, 1999 this sequence version replaced gi:5001502.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0372J12

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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RP11-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanesse, J.J. and de Jong, P.V. (1996) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-140K4, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-372J12. actual end is at base position 35689 of RP11-140K4.

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3167..3206
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repeat_region
3391..3690
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repeat_region
3767..4048
/rpt_family="Alu"
repeat_region
4049..4068
/rpt_family="TAAAA)n"
repeat_region
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/rpt_family="L1"
repeat_region
4452..4689
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4690..4991
/rpt_family="Alu"
repeat_region
4992..5055
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5060..5082
/rpt_family="TTTAA)n"
repeat_region
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/rpt_family="Alu"
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5367..6064
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repeat_region
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Db 132029 GGGGGGTTCTCTTATTTCTTAAGTTTATCTGAATCTCTGGGGAGTGCATGCCCAT 131970
Oy 2232 gtgcgaataaggagctctccctcctcagatcctcccatcctcagtttccctccatgaag 2291
Db 131969 GTTGAATATGAGTCTCTGCGCCTGAGATCTTCCCATCTCAGTTTCTTCCATGAAG 131910
Oy 2292 agtacgttaataacatagtgctc 2315
Db 131909 ACTACCTTAATACATACACTCTTC 131886

RESULT 11
AX003085 799 bp DNA PAT 24-AUG-2000
DEFINITION Sequence 5 from Patent EP0933425.
ACCESSION AX003085
VERSION AX003085.1 GI:9926966
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 799)
AUTHORS Michalovich,D. and Doe,T.R.
TITLE Semaphorin family polypeptides and polynucleotides
JOURNAL Patent: EP 0933425-A 5 04-AUG-1999;
SMITHKLINE BEECHAM PLC (GB)
FEATURES
Source 1..799
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 174 a 237 c 216 g 171 t 1 others
ORIGIN

Query Match 26.9%; Score 623; DB 9; Length 799;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 773; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 487 cgaccacaagaatcgcagcagtgctgaatggtccctcagagaactaaacatgacgac 546
Db 1 CGACCACAAGACATTCGAGCATGCTGATGCTCCCTTCAGAGAACTAAACATGACTGC 60
Oy 547 aacagaagagctcgtcgtgacaaatgagtgtcccaagccagaccttgagagatgacac 606
Db 61 AACACAGGACTCCTGCTGCGACATGATGTCGCCACCCAGACCTGAGAGTGCATC 120
Oy 607 accaacaacataaagctcgcgacacttgctcctcctcctcctcctcctcctcctcctc 666
Db 121 ACCAACACATACATACCTCCGACATTTGGCTCATCTCTCTCCCTCCCTGACCGCTACTC 180
Oy 667 accctcatccgagacacacacacacacacacacacacacacacacacacacacacacac 726
Db 181 ACCTTCATCCGGGACACCCACTCATGAGACAGCCAGTGTTCAGAGTATGAGCCACCC 240
Oy 727 ctgctgtcactacagatacagactatctcagatcgtgtgcccacaaggtgacagcctc 786
Db 241 CTGCTGTGCTACACAGTATACACCTATCTCAGAGTCTGCGCCACAGGCTGACCAAGCTTC 300
Oy 787 lcaaggagaagatlatgagtgctctacacctgggagacagagatgagacactccacagaga 846
Db 301 TCAGGGAAGAGATATGATGCTCTTACCTGGGACAGAGATGAGACACTCCACCCAGACA 360
Oy 847 gtgcgagatcgagctcagctcagcgttcttgagaatctgacctatccacagagcacag 906
Db 361 GTGCGAGATCGAGGCTCAGCTCAGCTTCTTGAAGATCTGGCTTATTCACAGCCACAG 420
Oy 907 ccaagtggagaacatgaatctgtacacagcgtgctcctggtgtgctccctacatagatg 966
Db 421 CCAGTGTGAGAACATGAATTTGTACACACAGCTGCTCTGTGTTGGCTCCGCTACTGAGTG 480
Oy 967 acacaaggaataacacacacacacacacacacacacacacacacacacacacacacac 1026

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|||||
Db 481 ACACAGTAATACACACACAGTGTGCGCTCTCCAGAGTGTCCAGAGTCAATCCGCGCC 540
Oy 1027 caggaccagctctgtcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1086
Db 541 CAGGACCGAGTCTGTGCTCCGAGAGCTTCCGCGGAGATGATGTGCGCCATCCGCGGAG 600
Oy 1087 caccgagaggtgtgctcacaagacatagatgacagatgctcctcctcctcctcctcctc 1146
Db 601 CACCGAGGCTGTGCTCCAGACATAGAGTACAGATGCTCTCTGTTGCTCTGAGAGAG 660
Oy 1147 cctggaagaacgtccagatggtttgaagttcccggtgagcagcagcgtgagatgctgtg 1206
Db 661 CCTGGAGAGCTCCAGTATGTTGAAGTTCCTGCGGCTACAGCTCCGATGTGCTT 720
Oy 1207 ccaatgtctcacaagcagacatgagcactcgtgtgtgacacacagccagatgagat 1262
Db 721 CCATGTTCTCAAGCTCAGCATGAGGATCTCTGTGTGCGACACAGCCAGCTGAGAGT 776

RESULT 12
AL451003 171964 bp DNA HTG 24-JAN-2001
LOCUS Homo sapiens chromosome 1 clone RP11-136B23, *** SEQUENCING IN
DEFINITION PROGRESS *** 18 unordered pieces.
ACCESSION AL451003 AC026541
VERSION AL451003.1 GI:11595430
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 171964)
AUTHORS Pavitt,R.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba136b23
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 163308 bases at least Q40
Consensus quality: 166597 bases at least Q30
Consensus quality: 168551 bases at least Q20
Insert size: 170264; sum-of-ctrls
Insert size: 177633; 11.9% error; agarose-tp
Quality coverage: 4.17x in Q20 bases; sum-of-ctrls Quality
coverage: 4.10x in Q20 bases; agarose-tp
-----
Draft Sequence Produced by Whitehead Institute/MIT Center for
Genome Research, 320 Charles Street,
Cambridge, MA 02141, USA.
http://www-seq.wi.mit.edu.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 3477: contig of 3477 bp in length
* 3478 3577: gap of 100 bp
* 3578 13586: contig of 10009 bp in length
* 13587 13686: gap of 100 bp

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* 13687 18688: contig of 5002 bp in length
* 18689 18788: gap of 100 bp
* 18789 26165: contig of 7377 bp in length
* 26166 26265: gap of 100 bp
* 26266 52879: contig of 26614 bp in length
* 52880 52979: gap of 100 bp
* 52980 82107: contig of 29128 bp in length
* 82108 82207: gap of 100 bp
* 82208 88054: contig of 5847 bp in length
* 88055 91774: contig of 3620 bp in length
* 91775 91874: gap of 100 bp
* 91875 101902: contig of 10028 bp in length
* 101903 102002: gap of 100 bp
* 102003 109337: contig of 7335 bp in length
* 109338 109437: gap of 100 bp
* 109438 113399: contig of 3962 bp in length
* 113400 113499: gap of 100 bp
* 113500 118719: contig of 5220 bp in length
* 118720 118819: gap of 100 bp
* 118820 123815: contig of 4996 bp in length
* 123816 123915: gap of 100 bp
* 123916 132492: contig of 8577 bp in length
* 132493 132592: gap of 100 bp
* 132593 137709: contig of 5117 bp in length
* 137710 137809: gap of 100 bp
* 137810 149420: contig of 11611 bp in length
* 149421 149520: gap of 100 bp
* 149521 156195: contig of 6675 bp in length
* 156196 156295: gap of 100 bp
* 156296 171964: contig of 15669 bp in length.
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FEATURES

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misc_feature
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ORIGIN
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Best Local Similarity 100.0%; Pred. No.5.2e-118;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 599 agtgcaccacaaacatgaagctccgcacattggctcctctctcctcgtcgtacc 658
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|||||
QY 659 ggcgtactaaccttcacccgcagaccacccactcaltgacagcagtglttccagctatg 718
|||||
Db 107911 GCGTACACACCTTCATCCGGGACACCCACCATCATGAGACAGCCAGTGTTCACATGATG 107970
|||||
QY 719 gccacccccctgctgtactacacagatcacgtctcttcagagtgctgtgcccacaggtga 778
|||||
Db 107971 GCCACCCCTGCTGCTGCTACATACAGCTATCTCAGAGTGTGTGCCACAGGGTGA 108030
|||||
QY 779 ccaagccctcagaggaagatgatgtctctcctcctcagggagacag 823
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RESULT 13

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LOCUS Homo sapiens chromosome 1 clone RP11-136B23 map 1, WORKING DRAFT
DEFINITION
SEQUENCE, 24 unordered pieces.
AC026541
VERSION AC026541.1 GI:7283245
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 172010)
Birken,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 1, clone RP11-136B23
JOURNAL Unpublished
2 (bases 1 to 172010)
Birken,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Bouckhalter,B., Brown,A., Burkett,G.,
Campiano,A., Castle,A., Choquel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodgson,S., Domingo,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,
Meldrum,J., Menus,L., Mihova,T., Miranda,C., Menga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisan,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rotman,D.,
Roy,A., Santos,R., Schauer,S., Severy,S., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessier,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,R., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
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TITLE Direct Submission
JOURNAL Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
```


✓

ORGA

LOCUS	AB047604	2669 bp	mRNA	PRI	01-SEP-2000
DEFINITION	Macaca fascicularis brain cDNA, clone:Ompa-10727.				
ACCESSION	AB047604				
VERSION	AB047604.1 GI:9929942				
KEYWORDS	fis (full insert sequence).				
SOURCE	Macaca fascicularis adult male brain parietal lobe cDNA to mRNA, clone:lib:macaque brain cDNA library Ompa clone:Ompa-10727.				
ORGANISM	Macaca fascicularis				
REFERENCE	Euhayota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.				
AUTHORS	1 (sites)				
TITLE	Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.				
JOURNAL	Isolation of full-length cDNA clones from macaque brain cDNA libraries				
REFERENCE	Unpublished (2000)				
AUTHORS	2 (bases 1 to 2669)				
TITLE	Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.				
JOURNAL	Direct Submission				
COMMENT	Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases.				
	Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail: khashi@nih.go.jp).				
	URL: http://www.nih.go.jp/iyoken/genbank/				
	Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)				
	Lab host: TOP10				
	Vector: pME18S-FL3 (Acc. No. AB009644)				
	R. Site1: DraIII (CAGCTGCGC)				
	R. Site2: DraIII (CAGCATGTC)				
	Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGTCGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' end primer [CTTCTGCTCTTAAGCTCGG]; 3' end primer [CGACCTCGAGCTGACGACCA]).				
FEATURES	Location/Qualifiers				
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	/db_xref="taxon:9541"				
	/clone="Ompa-10727"				

CDS
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/dev_stage="adult"
/sex="male"
/tissue_type="brain parietal lobe"
348..794
/codon_start=1
/product="hypothetical protein"
/protein_id="BAB12128.1"
/db_xref="GI:9929943"
/translation="MGAYACBCEGGAARVVAAYSLWGSQRDAPSRHTVAGLAGE
FLGVLAASLTLLIGRROORRRELRLARDKVLGLGAPSGTTSYSODPPSPPEDE
RLPLALAKRSGSGFSGFPFLDPCPSPAHRLRLTGAPLATCDETSL"

BASE COUNT 587 a 669 c 710 g 703 t
ORIGIN

Query Match 6.9% Score 159; DB 85; Length 2669;
Best Local Similarity 99.2% Pred No. 8.2e-80;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1550 tggacctgggggtccacacctctgggaccacaaagctacagccaagaccctccctccct 1609
DB 580 tggacctgggggtccacacctctgggaccacaaagctacagccaagaccctccctccct 639
QY 1610 ctccctgaagaatgagcggttgcgcgtggccctggccaagaaggagtggtcttgatgaa 1669
DB 640 ctccctgaagaatgagcggttgcgcgtggccctggccaagaaggagtggtcttgatgaa 699
QY 1670 tctcaccaccctctcgtcttgatccttggccaagcccaagcccaatctgggttaactgggg 1729
DB 700 tctcaccaccctctcgtcttgatccttggccaagcccaagcccaatctgggttaactgggg 759
QY 1730 ctcccttagccacatgtgaatgaacatccatctagagctgggcaaatgaaccatagtgta 1789
DB 760 ctcccttagccacatgtgaatgaacatccatctagagctgggcaaatgaaccatagtgta 819
QY 1790 taagtgatcaactggaaacggag 1810
DB 820 taagtgatcaactggaaacggag 840

Search completed: May 12, 2001, 18:39:43
Job time: 38184 sec

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1. 407
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/db_xref="taxon:9606"
/clone_lib="Soares_NhMpu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHM, and fetal heart NBHM19M) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT 118 a 106 c 96 g 87 t
ORIGIN

Query Match 14.0%; Score 325; DB 18; Length 407;
Best Local Similarity 100.0%; Pred. No. 8.5e-164;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1991 aatcagagctcccccacacatctgaactcctgtaacctatccctgccccctatc 2050
Db 335 AATCAGGGCTTCCCTTAACATCTGACTGTAACCTTATCCCTGCCCCCTATC 276
Qy 2051 ttggagccatagttttggagatggagcagagggcatagctatgcttctggtt 2110
Db 275 TTGGGCCCATTAAGTTTGGGAGATGGCGCACAGGCGATGACTATGACTTCTTGTGTT 216
Qy 2111 gggagccctggccggaagaagagccctggaggggtgttggggggaagagtgccctgaagtcct 2170
Db 215 GGAGCCTGGCCGGAAGAGAGCCCTGGAGGTGTGGGGGCAAAATGTGCCCTGAGTCTT 156
Qy 2171 tggagtgatctcctcattcctcaagttcattcgaactcgtgtggagtgatgatcccca 2230
Db 155 TGGGCTGGTTCCTTATCTTCAATTTATCTGAATCTGTGGGAGTGGATATGCCCA 96
Qy 2231 tgttgaatatggagtcctcctgagatcctcccatcagtttccctccatgaa 2290
Db 95 TGTTCGAATATGAGTCTGTGCGCTGAGATCTCCCATCTCAAGTTTCTCCATCATGAA 36
Qy 2291 gagtagtgtaaatatagtggtc 2315
Db 35 GAGTACGTGAATACATAGTGTTC 11

RESULT 8
LOCUS H24181 437 bp mRNA EST 06-JUL-1995
DEFINITION ym55f02.r1 Soares Infant Brain INTB Homo sapiens cDNA clone
IMAGE:52280 5' similar to SP:A49069 A49069 COLAPSPIN - ; mRNA
sequence.
ACCESSION H24181
VERSION H24181.1 GI:892876
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 437)
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maria, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
JOURNAL
COMMENT Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 1989
High quality sequence stops: 310 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1989 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 310.
Location/Qualifiers
1. 437
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/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lambda B; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5', AACTGGAAGATTCGGCGCCGAGGATTTTATTTTATTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lambda B vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 105 a 122 c 112 g 95 t 3 others
ORIGIN

Query Match 12.9%; Score 298; DB 153; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.3e-149;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 488 gaccacaagacatcggacagtgctgaatgctcctcctcagagaactaaacatgactgca 547
Db 1 GACCACAAAGACATTCGGACAGTCTGATAGTCCCTTCAAGAACTAAACATGACTGCA 60
Qy 548 acaagagagctgctctgtgtgacaatgattgcccacagcccaactcggagatgactca 607
Db 61 ACAGAGAGACGCTGTGCTGTGACAAATGATGTGCCCAAGCCCAAGCTGGAGATGATCA 120
Qy 608 ccaacaacatgagagctcccgacacttggctcattctctcctcctgacctgagcgtactca 667
Db 121 CCACACATGAAAGCTCCGCACTTGGCTCATCTCTCTCCCTGCGAGCGGTACTCA 180
Qy 668 ccttaccgagacacacccatcatgagcagcagtgcttccagctgtagtgcaccccc 727
Db 181 CCTTATCCGGGAGACACCCACTATGGACAGCGAGTGTTCAGCTGATGGCCACCCCC 240
Qy 728 tgcctgtactacagatacagcctatctcagagtcgtgtgcccacaggggtgacacgct 785
Db 241 TCGTGTCTACTACAGATACAGAGCTATCTCAGAGTCTGCGCCACAGGTTGACCAAGCT 298

RESULT 9
LOCUS BE734978 1045 bp mRNA EST 15-SEP-2000
DEFINITION 601570573.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3844914 5',
mRNA sequence.
ACCESSION BE734978
VERSION BE734978.1 GI:10149073
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1045)
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="1877444"
/clone_lib="Source_NhnpU_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
lab_host="DH10B"

```

were made *in vitro*. Following HAP purification, phos DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 480048-326470, and 484486-488070.

BASE COUNT	118 a	106 c	96 g	87 t
ORIGIN				

```

Query Match      14.0%; Score 325; DB 18; Length 407;
Best Local Similarity 100.0%; Pred. No. 8.5e-164;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Qy 1991 aaatcagagcctccccctaacatctgaactcctgtaaacctcatccctgccccctatc 2050
|||||
Db 335 AATTCAGGCTTCCCCCTAACATCTGAGACTCCTGTAAACCTTCATCCTGGCCCCCTATC 276

[illegible]

QY 2111 ggaagcctggccggaaggaagagccctggaggtggtctgggggcaaatctgtccctgagtcct 2170
Db 215 ggaacctggccgggaaggaagagccctggaggtggtctgggggcaaatctgtccctgagtcct 156

QY 2171 tggggtggtctgcgtatctctcaagttatctgaatctgtgggagtcgatcccca 2230
|||||
Db 155 TGGGGTGGTCTGCCTTATCTTCAAGTTATCTGATCTGTGGGAGTCGATATCCCA 96
|||||

OY 2231 tgttgcacatcagtagctctcgccctgagatcttcccactcaagtlttcctccatgaaa 2300
|||||
95 TGTTCGAATATGGAGCTCTCTGCCCTGAGATCTTCCCACATCTCAGTTTCCCTTCATGA 36

Qy 2291 gagtaacgtgtaaatatcatagttc 2315
|||||
Db 35 GAGTACGTGTAATAATACATAGTCTC 11

LOCUS	437 bp	EST	06-JUL-1995
DEFINITION	ym55f02.r1 Soares infant brain INTB Homo sapiens cDNA clone		

ACCESSION	H24181	
VERSION	H24181.1	GI:892876
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM	REFERENCE
Homo sapiens	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, I. (bases 1 to 437)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	

TITLE	The Washu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Robert Storz, 1998

High quality sequence strop: 310 Source: IMAGE Consortium, LNLN
This clone is available royalty-free through LNLN ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1989 Std Error: 0.00
Seq primer: M13Rp1
High quality sequence strop: 310

FEATURES

SOURCE

Location/Qualifiers
1. .437

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/organism="Homo sapiens"
/db_xref="GDB:425216"
/db_xref="taxon:9606"
/clone IMAGE:52280"
/clone_1b="Soares Infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: latmid BA; Site: 1; Not
I; Site2: Hind III; 1st strand cDNA was primed with a Not
I - oliga(dt) primer (5'
AATCGAAGAATTCGCGCCGACGAAATTTTTTTTTTTT 3') ;
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the latmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

```

Query Match	12.9%	Score 298:	DB 153:	Length 437:
Best Local Similarity	100.0%	Pred. No.	3.3e-149:	
Matches 298:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:

Oy 488 gaccacaagacattctgcagactgctgaatgtgcccttcagaagaacttaaaacttgactcyca 547
|||||
Db 1 GACCACAAGACATTTCGACAGTCTGAATGGTCCCTTCAGAAGACTAAAACATGACTCGCA 60

QY 548 acagagactgcctctgcgtgacaaatgatctgcccagcccaagacctgtgagagtgatca 607
|||||
Db 61 ACAGAGGACTTCCTCTGCTGGACAATGATCTGCCCCAGCCAGACCTGGAGAGTGCATCA 1202

QY 608 ccaacaacatgaagctccgcgcaatttggtcatctctctccctgactgacgcgactaca 666
|||||
Db 121 ccaacaacatgaagctccgcgcaatttggtcatctctctccctgactgacgcgactaca 180

QY 668 ccttcatccgagaccaccatctatgacagcgccagtgtcttcacagtatgacacccc 72
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Db 181 cctttatccgggacaccaccatctatggacagggccagtgtttccagcgtgatggccacccc 24

[illegible]

RESULT 9

LOCUS	1045 bp	EST	15-SEP-2000
DEFINITION	BE734978	601570573F1	NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3844914 5'
	mRNA sequence.		

ACCUSSION	2875278	GI:10149073
VERSION	BE734978.1	
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM	REFERENCE
Homo sapiens	1 (bases 1 to 1045)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
Eumetazoa; Eumetazoa; Primates; Catarrhini; Hominoidea; Homo.	

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2001, 10:33:52 ; Search time 454.55 Seconds

(without alignments)
5147.499 Million cell updates/sec

Title: US-09-284-180-1

Perfect score: 4008

Sequence: 1 gccgagggccgcgcagtagc.....aaaaaaaaaaaaaaaa 4008

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 678276 seqs, 291890651 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_0401.*

1: /cgnl_8/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseq/NA1983.DAT.*
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11: /cgnl_8/gcgdata/geneseq/geneseq/NA1990.DAT.*
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21: /cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /cgnl_8/gcgdata/geneseq/geneseq/NA2001.DAT.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4008	100.0	4008	19	V07279 Rat semaphorin W e
2	2331	58.2	2331	19	V07280 Rat semaphorin W e
3	107	2.7	4024	21	V07282 Mouse semaphorin W e
4	75	1.9	1761	19	V07282 Human semaphorin W e
5	75	1.9	2315	19	V07281 Human semaphorin W e
6	75	1.9	2893	20	X86126 DNA encoding SBSEM
7	75	1.9	2894	20	X86127 EST sequence for D
8	54	1.3	799	20	X86128 EST sequence for D
9	48	1.2	3821	15	O56609 Human PGF-2/WF-3
10	48	1.2	3821	20	X34365 Human nerve growth
11	48	1.2	11832	19	V21148 Nucleotide sequenc

C	12	47	1.2	160	19	V16145	Microsatellite mar
C	13	47	1.2	338	20	Z20475	Barley microsatell
C	14	46	1.1	73	13	O34140	Sequence of a micr
C	15	46	1.1	177	20	X61217	DOA1-DQB1 target r
C	16	46	1.1	261	18	T65656	Polymorphic repeat
C	17	46	1.1	307	21	A35342	Mytilus microsat
C	18	46	1.1	367	20	Z27707	Human DNA marker C
C	19	46	1.1	1131	20	Z28294	Rat neuronal limed
C	20	46	1.1	1344	20	X97975	Human secreted pro
C	21	46	1.1	2385	21	A39981	Human TANGO 187 c
C	22	46	1.1	2403	21	A39953	Human TANGO 187-1/
C	23	46	1.1	2418	21	A39979	Human TANGO 187-2/
C	24	46	1.1	2446	16	T08768	Rat biglycan cDNA
C	25	46	1.1	2490	21	A39975	Human TANGO 187-1/
C	26	46	1.1	2523	21	A39978	Human TANGO 187-1/
C	27	46	1.1	2562	21	A39980	Human TANGO 187-3/
C	28	46	1.1	2595	21	A39976	Human TANGO 187-2/
C	29	46	1.1	2614	19	V65766	Rat progression el
C	30	46	1.1	2614	20	Z23030	Rat progression el
C	31	46	1.1	2700	21	A39977	Human TANGO 187-1/
C	32	46	1.1	3120	14	O39261	Human t-complex as
C	33	46	1.1	3358	19	V58005	Rat neuritin rece
C	34	46	1.1	3358	21	Z91457	Rat neuritin rece
C	35	46	1.1	3809	12	Q12760	P40 genomic DNA
C	36	46	1.1	35828	21	A29063	Murine TGF-beta b1
C	37	46	1.1	44576	21	Z61522	Cosmid CVO14 conta
C	38	46	1.1	44848	21	A75080	Nucleotide sequenc
C	39	46	1.1	45546	20	X23520	Human kidney amino
C	40	45	1.1	56	18	T65796	Repeat sequence fr
C	41	45	1.1	175	18	T65655	Polymorphic repeat
C	42	45	1.1	214	18	T65688	Polymorphic repeat
C	43	45	1.1	241	20	Z20471	Barley microsatell
C	44	45	1.1	260	20	Z20469	Barley microsatell
C	45	45	1.1	262	21	A43685	Human secreted exp

ALIGNMENTS

RESULT	1	
V07279		
ID	V07279	standard: cDNA to mRNA: 4008 BP.
XX		
AC	V07279;	
XX		
DT	08-SEP-1998	(first entry)
XX		
DE	Rat semaphorin W encoding cDNA with 5' UTR and 3' UTR.	
XX		
KW	Rat; semaphorin W; nerve extension inhibitor; antiallergic; anticancer;	
KM	immunosuppressant; gene therapy; diagnosis; research reagent; ds.	
XX		
OS	Rattus norvegicus.	
XX		
FH	Key.	
FT	5' UTR	Location/Qualifiers
FT		1..75
FT		/*tag= a
FT	CDS	76..2406
FT		/*tag= b
FT		/product= "semaphorin W"
FT	5' UTR	2407..3977
FT		/*tag= c
FT		3978..4008
FT		/*tag= d
PN	W09815628-A1.	
PD	16-APR-1998.	
XX		
XX	03-OCT-1997;	97MO-JP03549.
XX		
PR	09-OCT-1996;	96JP-0287636.
XX		

[illegible]

QY	2881	tgvggagatcgagagagaaaggtcttggaatvggvgagcaacttaacccctcgtagccagtagag	2940
Db	2881	tgvggagatcgagagagaaaggtcttggaatvggvgagcaacttaacccctcgtagccagtagag	2940
QY	2941	gaaacacaaatgcgcgtcccccatacccaacagagcctcttaactcttagacaaagtcc	3000
Db	2941	gaaacacaaatgcgcgtcccccatacccaacagagcctcttaactcttagacaaagtcc	3000
QY	3001	aaagtgaacctctggtgtggaaagagcagagacaatgtagcccccgtctctctctgtc	3060
Db	3001	aaagtgaacctctggtgtggaaagagcagagacaatgtagcccccgtctctctctgtc	3060
QY	3061	ttccctctctgagcccaacacatgcgcgtgagccacgcctgagcttccctcgagtagag	3120
Db	3061	ttccctctctgagcccaacacatgcgcgtgagccacgcctgagcttccctcgagtagag	3120
QY	3121	agagcgaatccctctgctccctctggtcttcacatctaaatgaaacttcacaacatctaaat	3180
Db	3121	agagcgaatccctctgctccctctggtcttcacatctaaatgaaacttcacaacatctaaat	3180
QY	3181	ggggagatgacaatgacctttttccccaagaagaatggttagaataacaaagcagttaa	3240
Db	3181	ggggagatgacaatgacctttttccccaagaagaatggttagaataacaaagcagttaa	3240
QY	3241	gaagattgagcctcagtgaaacttcaaccccttgagcaagagatccctcagctagagtc	3300
Db	3241	gaagattgagcctcagtgaaacttcaaccccttgagcaagagatccctcagctagagtc	3300
QY	3301	tgtagaactccctgaaatctgatactgcctgtagaactccctgaaatctgatactgata	3360
Db	3301	tgtagaactccctgaaatctgatactgcctgtagaactccctgaaatctgatactgata	3360
QY	3361	gtggt	3420
Db	3361	gtggt	3420
QY	3421	gt	3480
Db	3421	gt	3480
QY	3481	tatagtaacacacacttgagccacaatgagagagatgtgtgtgtgtgtgtgtgtgtgt	3540
Db	3481	tatagtaacacacacttgagccacaatgagagagatgtgtgtgtgtgtgtgtgtgtgt	3540
QY	3541	ggagcagccttgagggcagccccccttgagcaacatgtgtgtgtgtgtgtgtgtgtgt	3600
Db	3541	ggagcagccttgagggcagccccccttgagcaacatgtgtgtgtgtgtgtgtgtgtgt	3600
QY	3601	cttggaagctagagctctgagcggtgactgaaagagacacacatctccctctgtctaatc	3660
Db	3601	cttggaagctagagctctgagcggtgactgaaagagacacacatctccctctgtctaatc	3660
QY	3661	tcctgt	3720
Db	3661	tcctgt	3720
QY	3721	cctgt	3780
Db	3721	cctgt	3780
QY	3781	ctgctctcccttgaaagcagcctgtagaacatactaaagatccctctggtcttgagattccg	3840
Db	3781	ctgctctcccttgaaagcagcctgtagaacatactaaagatccctctggtcttgagattccg	3840
QY	3841	gtgagcttgagtaagacatcttgagcgtagacatcaaacctgacagatgtagcttcatgt	3900
Db	3841	gtgagcttgagtaagacatcttgagcgtagacatcaaacctgacagatgtagcttcatgt	3900
QY	3901	aaagtvggagatactactcctcagaggtgtgctgcaagatcaaacagagaaacgtataat	3960
Db	3901	aaagtvggagatactactcctcagaggtgtgctgcaagatcaaacagagaaacgtataat	3960

[illegible]

ID	287977
XX	287977 standard; DNA: 4024 BP.
AC	287977:
XX	
DT	05-JUN-2000 (first entry)
XX	
DE	Mouse semaphorin W polypeptide encoding DNK.
KW	Semaphorin W gene; hereditary disease; Parkinson's disease; mouse; ds.
XX	
OS	Mus musculus.
XX	
FH	Key Location/Qualifiers
FT	CDS 79..2412
PT	/tag= a
XX	
PN	WO20006725-A1.
XX	
PD	10-FEB-2000.
XX	
PF	30-JUL-1999; 99WO-JP04120.
XX	
PR	31-JUL-1998; 98JP-0217467.
PR	24-FEB-1999; 99JP-0046833.
XX	
PA	(SUMU) SUMITOMO PHARM CO LTD.
XX	
PI	Kimura T, Enclinas JA;
DR	WPI: 2000-195293/17.
DR	P-PsDB: Y77803.
XX	
DI	Diagnosis of hereditary diseases such as Parkinson's disease by analyzing the occurrence of mutation in the semaphorin W gene, or determining the genotype of the semaphorin w gene in an individual -
XX	
PS	Disclosure; Page 22-28; 40pp; Japanese.
CC	The invention provides a method for diagnosing or determining hereditary diseases by analyzing the occurrence of mutation in the semaphorin W gene. The semaphorin W gene is useful for the diagnosis of hereditary diseases such as Parkinson's, and for determining the genotype of the semaphorin W gene in an individual. The present sequence represents a DNA encoding a mouse semaphorin W polypeptide.
SO	Sequence 4024 BP; 768 A; 1128 C; 1172 G; 956 T; 0 other;
<hr/>	
Query Match	2.7%; Score 107; DB 21; Length 4024;
Best Local Similarity	99.4%; Pred. No. 1.le-30;
Matches 157; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	511 ggcacccttcgctttgatccgaagtgcgggttatttgatgtgccaggtttccacgaaggc 570 Db 517 ggcaccttcgctttgatccgaagtgcgggttatttgatgtgccaggtttccacgaaggc 576 OY 571 gaagaacttgaaagcgccggggggaatgtccttttgagccagctcaacggttcagcagct 630 Db 577 gaagaacttgaaagcgccggggggaatgtccttttgagccagctcaacggttcagcagct 636 631 gtaatgctlgggggtctcctctacaacgcacattgaaa 668 Db 637 gtaatgctlgggggtctcctctacaacgcacattgaaa 674
<hr/>	
RESULT	4
V07282	V07282 standard; cDNA to mRNA; 1761 BP.
AC	V07282:
XX	
DT	08-SEP-1998 (first entry)

```

XX Human semaphorin W encoding cDNA.
DE
XX
XX Human; semaphorin W; nerve extension inhibitor; antiallergic; anticancer;
KW Immunosuppressant; gene therapy; diagnosis; research reagent; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1764
XX FT /*tag= a
XX FT /product= "semaphorin W"
XX
XX MO9815628-A1.
XX
XX 16-APR-1998.
XX
XX 03-OCT-1997; 97WO-JP03549.
XX
XX 09-OCT-1996; 96JP-0287636.
XX
XX (SUMU ) SUMITOMO PHARM CO LTD.
XX
XX Kikuchi K, Kimura T;
XX WPI: 1998-261015/23.
XX P-PSDB: W51314.
XX
XX Nerve extension inhibitor protein semaphorin W - is useful as
XX therapeutic drug and diagnostic and research reagent
XX
XX Claim 2; Page 67-68; 90pp; Japanese.
XX
XX The present sequence encodes human semaphorin W. Semaphorin W and
XX its derivatives are nerve extension inhibitors which are useful as
XX antiallergic, immunosuppressant and anticancer agents. The DNA
XX encoding semaphorin W can also be used in gene therapy, e.g. using
XX a viral vector. The proteins, peptides, DNA and antibodies which
XX recognise the protein or peptides, can be used as diagnostic or
XX research reagents. Semaphorin W can be used as a screen for
XX semaphorin W antagonists with possible therapeutic use.
XX
XX Sequence 1761 BP; 349 A; 511 C; 521 G; 380 T; 0 other.
XX
XX
XX Query Match 1.9%; Score 75; DB 19; Length 1761;
XX Best Local Similarity 100.0%; Pred. No. 8.1e-19;
XX Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1362 cccctgtgtgctactacagatcctatctcagagtcgtgcccacaggtgaccag 1421
DB 723 cccctgtgtgctactacagatcctatctcagagtcgtgcccacaggtgaccag 782
OY 1422 cctctcagggaaga 1436
DB 783 cctctcagggaaga 797
XX
XX
XX RESULT 5
XX V07281
XX ID V07281 standard; cDNA to mRNA; 2315 BP.
XX
XX V07281;
XX
XX 08-SEP-1998 (first entry)
XX
XX Human semaphorin W encoding cDNA with 3'UTR.
XX
XX Human; semaphorin W; nerve extension inhibitor; antiallergic; anticancer;
KW Immunosuppressant; gene therapy; diagnosis; research reagent; ds.
XX
XX Homo sapiens.
XX

```

```

FH Key Location/Qualifiers
FT CDS 1..1764
FT FT /*tag= a
FT FT /product= "semaphorin W"
FT FT 5'UTR 1765..2315
FT FT /*tag= b
XX
XX MO9815628-A1.
XX
XX 16-APR-1998.
XX
XX 03-OCT-1997; 97WO-JP03549.
XX
XX 09-OCT-1996; 96JP-0287636.
XX
XX (SUMU ) SUMITOMO PHARM CO LTD.
XX
XX Kikuchi K, Kimura T;
XX WPI: 1998-261015/23.
XX P-PSDB: W51314.
XX
XX Nerve extension inhibitor protein semaphorin W - is useful as
XX therapeutic drug and diagnostic and research reagent
XX
XX Claim 2; Page 65-66; 90pp; Japanese.
XX
XX The present sequence encodes human semaphorin W. Semaphorin W and
XX its derivatives are nerve extension inhibitors which are useful as
XX antiallergic, immunosuppressant and anticancer agents. The DNA
XX encoding semaphorin W can also be used in gene therapy, e.g. using
XX a viral vector. The proteins, peptides, DNA and antibodies which
XX recognise the protein or peptides, can be used as diagnostic or
XX research reagents. Semaphorin W can be used as a screen for
XX semaphorin W antagonists with possible therapeutic use.
XX
XX Sequence 2315 BP; 463 A; 640 C; 670 G; 542 T; 0 other.
XX
XX
XX Query Match 1.9%; Score 75; DB 19; Length 2315;
XX Best Local Similarity 100.0%; Pred. No. 7.7e-19;
XX Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1362 cccctgtgtgctactacagatcctatctcagagtcgtgcccacaggtgaccag 1421
DB 723 cccctgtgtgctactacagatcctatctcagagtcgtgcccacaggtgaccag 782
OY 1422 cctctcagggaaga 1436
DB 783 cctctcagggaaga 797
XX
XX
XX RESULT 6
XX X86126
XX ID X86126 standard; DNA; 2893 BP.
XX
XX X86126;
XX
XX 15-SEP-1999 (first entry)
XX
XX DNA encoding SBSEMN1, a semaphorin family polypeptide.
XX
XX SBSEMN1; semaphorin; neurodegeneration; spinal injury; neuropathy;
KW neuromuscular disorder; muscular dystrophy; psychiatric disorder;
KW inflammatory disorder; developmental malformation;
KW immune system disorder; cancer; viral infection; vaccine; ss.
XX
XX Homo sapiens.
XX
XX EP933425-A1.
XX
XX 04-AUG-1999.
XX

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PF 30-SEP-1998: 98EP-0203287.
XX
XX 30-JUL-1998: 98GB-0016676.
PR 30-JAN-1998: 98EP-0300693.
PR 28-JUL-1998: 98GB-0016423.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
PI Doe TR, Hayes PD, Michalovich D;
XX WPI: 1999-407151/35.
DR P-PSDB; Y23873.
XX
XX New semaphorin family polypeptide useful for treating spinal injury
PT and muscular dystrophy
XX
XX Claim 7: Page 13-14; 29pp; English.
XX
XX The present sequence encodes SBSEMN1, a semaphorin family polypeptide.
CC The polypeptide may be used to screen for agonists or antagonists
CC including antibodies. Measurement of the level of SBSEMN1 protein
CC and detection of a mutation in its polynucleotide may also be used to
CC diagnose a disease or condition or susceptibility to a disease related
CC to altered expression or activity of SBSEMN1. These diseases and
CC conditions include neurodegeneration, spinal injury, neuropathies,
CC neuromuscular disorders, muscular dystrophy, psychiatric disorders,
CC inflammatory disorders, developmental malformations, disorders of the
CC immune system, cancer and viral infections. The protein may also be
CC used to treat these diseases and conditions by administration as a
CC vaccine.
XX
XX Sequence 2893 BP; 579 A; 825 C; 842 G; 647 T; 0 other;
XX
SQ

Query Match
Best Local Similarity 1.9%; Score 75; DB 20; Length 2893;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1362 cccctgtgtgctactacagatacagcctatctcagagctgtgcccacagggtgaccag 1421
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DB 1282 cccctgtgtgctactacagatacagcctatctcagagctgtgcccacagggtgaccag 1341
|||
OY 1422 cctctcagggaaga 1436
|||
DB 1342 cctctcagggaaga 1356

RESULT 7
X86127
ID X86127 standard; DNA: 2894 BP.
XX
XX X86127;
AC
XX
DT 15-SEP-1999 (first entry)
XX
XX EST sequence for DNA encoding SBSEMN1.
DE
XX SBSEMN1: semaphorin; neurodegeneration; spinal injury; neuropathy;
KM neuromuscular disorder; muscular dystrophy; psychiatric disorder;
KM inflammatory disorder; developmental malformation; EST;
KW expressed sequence tag; immune system disorder; cancer;
KW viral infection; vaccine; ss.
XX
XX Homo sapiens.
OS
XX
XX EP933425-A1.
PN
XX
XX 04-AUG-1999.
PD
XX
XX 30-SEP-1998: 98EP-0203287.
PF
XX 30-JUL-1998: 98GB-0016676.
PR 30-JAN-1998: 98EP-0300693.
PR 28-JUL-1998: 98GB-0016423.
XX

PR 28-JUL-1998: 98GB-0016423.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Doe TR, Hayes PD, Michalovich D;
PI
XX WPI: 1999-407151/35.
DR P-PSDB; Y23874.
XX
XX New semaphorin family polypeptide useful for treating spinal injury
PT and muscular dystrophy
XX
XX Claim 18: Page 14-15; 29pp; English.
XX
XX The present sequence represents an expressed sequence tag (EST)
CC sequence, from which DNA encoding SBSEMN1, a semaphorin family
CC polypeptide, is derived. The polypeptide may be used to screen
CC for agonists or antagonists including antibodies. Measurement
CC of the level of SBSEMN1 protein and detection of a mutation in
CC its polynucleotide may also be used to diagnose a disease or
CC condition or susceptibility to a disease related to altered
CC expression or activity of SBSEMN1. These diseases and
CC conditions include neurodegeneration, spinal injury, neuropathies,
CC neuromuscular disorders, muscular dystrophy, psychiatric disorders,
CC inflammatory disorders, developmental malformations, disorders of the
CC immune system, cancer and viral infections. The protein may also be
CC used to treat these diseases and conditions by administration as a
CC vaccine.
XX
XX Sequence 2894 BP; 580 A; 824 C; 841 G; 646 T; 3 other;
XX
SQ

Query Match
Best Local Similarity 1.9%; Score 75; DB 20; Length 2894;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1362 cccctgtgtgctactacagatacagcctatctcagagctgtgcccacagggtgaccag 1421
|||
DB 1282 cccctgtgtgctactacagatacagcctatctcagagctgtgcccacagggtgaccag 1341
|||
OY 1422 cctctcagggaaga 1436
|||
DB 1342 cctctcagggaaga 1356

RESULT 8
X86128
ID X86128 standard; DNA: 799 BP.
XX
XX X86128;
AC
XX
DT 15-SEP-1999 (first entry)
XX
XX EST sequence for DNA encoding SBSEMN1.
DE
XX SBSEMN1: semaphorin; neurodegeneration; spinal injury; neuropathy;
KM neuromuscular disorder; muscular dystrophy; psychiatric disorder;
KM inflammatory disorder; developmental malformation; EST;
KW expressed sequence tag; immune system disorder; cancer;
KW viral infection; vaccine; ss.
XX
XX Homo sapiens.
OS
XX
XX EP933425-A1.
PN
XX
XX 04-AUG-1999.
PD
XX
XX 30-SEP-1998: 98EP-0203287.
PF
XX 30-JUL-1998: 98GB-0016676.
PR 30-JAN-1998: 98EP-0300693.
PR 28-JUL-1998: 98GB-0016423.
XX

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2001, 14:35:12 ; Search time 6014.38 seconds
(without alignments)
3362.619 Million cell updates/sec

Title: US-09-284-180-4

Perfect score: 2315

Sequence: 1 999999tctctctatgctgc.....cgtgtaaatacatagtgctc 2315

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 9623517 seqs, 4368049070 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	638	27.6	733	122	AW957134 EST369204
2	628	27.1	733	122	AW953466 EST365536
3	449	19.4	459	19	AI379133 tc59q09.x
4	401	17.3	456	104	AI942370 w080606.x
5	375	16.2	503	7	AA459837 zx50g12.r
6	345	14.9	534	165	BE273314 601142480
7	325	14.0	407	18	AI276851 q167g11.x
8	298	12.9	437	153	H24181 ym5f02.r1
9	294	12.7	1045	139	BE734978 601570573
10	260	11.2	394	153	H24073 ym54f02.s1
11	235	10.2	337	159	Z45329 ym08g07.s1
12	218	9.4	592	205	AO382219 EST06966.in
13	217	9.4	364	156	AO382219 CTTR1-E1-
14	211	9.1	413	152	H10410 ym08g07.s1
15	195	8.4	317	14	AA937917 of72e01.s
16	193	8.3	347	152	H10623 ym08g07.r1
17	193	8.3	517	155	R54387 yg78f12.r1
18	182	7.9	297	159	Z41043 HSC2MG092.n

C 19	168	7.3	285	7	AA460024
C 20	157	6.8	558	16	AA133725
C 21	135	5.8	307	155	R52120
C 22	113	5.1	233	152	F02243
C 23	112	4.8	469	120	AM838037
C 24	112	4.8	489	117	AM608110
C 25	112	4.8	489	117	AM608155
C 26	85	3.7	212	159	Z42773
C 27	71	3.1	290	152	F11335
C 28	71	1.5	376	115	AM436751
C 29	33	1.4	232	114	AM346693
C 30	33	1.4	232	114	AM346698
C 31	32	1.4	689	148	BF467265
C 32	30	1.3	522	138	BE667719
C 33	30	1.3	556	138	BE683223
C 34	24	1.0	208	115	AM436702
C 35	24	1.0	400	201	AC018630
C 36	22	1.0	418	147	BF392081
C 37	22	1.0	426	139	BE754071
C 38	22	1.0	430	157	T95289
C 39	22	1.0	482	147	BF392768
C 40	22	1.0	804	231	CNS033C6
C 41	22	1.0	929	231	CNS04R1V
C 42	22	1.0	955	231	CNS03JUN
C 43	21	0.9	407	225	AE661172
C 44	21	0.9	473	17	A1205835
C 45	21	0.9	475	227	B75268
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					R52120 y858707.s1
					F02243 HSC0TE022
					AM838037 QV3-LT00
					AM608110 QV3-LT00
					AM608155 QV3-LT00
					Z42773 HSC0TE021
					F11335 HSC2VBE071
					AM436751 77209 MA
					AM346693 29273 MA
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					BF467265 UI-M-CG0
					BE667719 155505 M
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					A1205835 q933f09.x
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AM608155	OV3-LT004		
242273	HSC0TE021.n		
F11335	HSC2VE071.n		
AM436751	77209.MAR		
AM346693	29273.MAR		
AM346698	29282.MAR		
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BE683223	182687.MA		
AM436702	77141.MAR		
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BF395081	UT-R-CAO-		
BE754071	2073368.MA		
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Db	71	AACCAACTGTGGCCGCTCCAGAGCTGTCCAGAGTGCATCTCGGCCACGAGACCAGTCTG	130
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Db	131	TGCGCTTGAGGCTTCGGCTGGATAGTGTGTGGCCATGCGCGGGAGACACGAGGTTGGT	190
Qy	1101	ccaagacataagatcagcaaatgtccctccctttgtgtcctaaagagccttgagaagctgc	1160
Db	191	CCAGACATAGAGTCACAGCAATCTCTCTTTGTGTCTCTAAAGAGCCTGGAGAACGCTC	250
Qy	1161	agtagtcttgaagttcccgctgagctacagctcgacatgtgctctgtccatgttcttccaaag	1220
Db	251	AGTAGTCTTTGAAGTTCCGCTGGCTGACTGAGCATGTGTGCTTGCCATGTCTTCCAAAG	310
Qy	1221	ctcagcatgggacatcctgtgtgtgtgacacagaccagttgagtactgaactcaaccaccg	1280
Db	311	CTCAGCATGGGACATCCGTCGTGTGTGGACACAGGCCAATGAGTACATGCACATCCACCCCG	370
Qy	1281	gcgggagtgaacttgaggtggtgtgtgtgaccccaaggagggcgcttatgctctgtgaatg	1340
Db	371	GCGGGATGCACTGGAGGTGTGTGTGTGACCCCAAGGGGCAATGGGCGCTTATGCTGTGAATG	430

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ACCESSION	EST369204
VERSION	AM957134
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SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 733) Hogde, P., Qi, R., Abernathy, K., Dharp, S., Gaspar, R., Gay, C., Holt, I.E., Seed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished (2000)
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johng@tigr.org Plate: 102
FEATURES	Seq primer: Reverse.
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	/db_xref="taxon:9606"
	/clone_lib="MAGE_ressequences, MAGD"
	/note="Vector: pBluescriptSkm"
BASE COUNT	134 a 204 c 238 g 157 t
ORIGIN	

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Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 688;	Conservative	0;	Mismatches 1;	Indels 0;
				Caps

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Db	71	AACCAACTGTGGCCGCTCTCCAGAGACTGCTCAGAGTAGCATCTCCGCCACGAGACCAGTCTG		130
OY	1041	tgccttgagagcttcaggcttgaatgaatgatgtgtgtgcccatgcgggggagacacggaggttgt		1100
Db	131	TGCCTGTGGAGCTTCGGCTGTGATAGTGTGTGTGGCCATGCGCGGAGCACCGAGGGTTGGT		190
OY	1101	ccaagacataagagtcacagcagaatblctccctctttgtgtlccctaagagccctggagaacctcc		1160
Db	191	CCAAGACATAGAGTCACACAGATGTCTCTTTTGTGTCTTAAGAACCTGGGAAGAGTCC		250
OY	1161	agtagtcttgaagtlcccgtygcctaacagctgcacatgtgtctcttccattgtctccaag		1220
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Db	371	GGGGATGTGAGCTGGAGGTGTGTGTGGACCCGAGGGGACATGGGGCTTAAGCTGTGAAG		430
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Db	551	TCTGCAGCATCCCTGTGACTCTCATTTGATTTGGTGTGGCGTCACACGACGACGACAGNA		610
OY	1521	ggaactctgtcgtcagaagaagtggtggcctgtgacccctgggggagctccacatctctgggagcc		1580
Db	611	GGAACTTCTGGCTAGAACACAGAAGTGGGCTCTGGACCTGGGGGCTCCACCTTCTTGGACAC		670
OY	1581	aagctacagcccaagaccctccctcccccct		1609
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VERSION	AM953466.1	GI:8143149		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 733)			
	Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,			
	I.E., Seeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and			
	Quackenbush,J.			
TITLE	Assessment of gene expression patterns in a model of colon tumor			
JOURNAL	metastasis using a 19,200 element cDNA microarray			
COMMENT	Unpublished (2000)			
	Contact: John Quackenbush			
	The Institute for Genomic Research			
	9712 Medical Center Dr., Rockville, MD 20850, USA			
	TEL: 301 838 3528			
	Fax: 301 838 0208			
	Email: johng@ligr.org			
	Plate: 51			

LOCUS	AW953466	733 bp	EST	01-JUN-2000
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ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 733)			
AUTHORS	Hagde,P., Ol,R., Abernathy,K., Dharp,S., Gaspar,R., Gay,C., Holm,I.E., Seed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.			
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johng@tigr.org Plate: 51			

```
FEATURES                      Seq primer: Reverse
                                Location/Qualifiers
                                1..733
                                /organism="Homo sapiens"
                                /db_xref="taxon:9606"
                                /clone.lib="MAGE resesquences, MAGB"
                                /note="Vector: pbluescriptskm"
BASE COUNT      133 a      207 c      238 g      154 t      1 others
ORIGIN

Query Match      27.1%; Score 628; DB 122; Length 733;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 921 gaaattgtacacacagctggctccttggtctccgctactgagtgagtcacaagtgaatc 980
Db 11 GAAATTGTACACACAGCTGGCTCCTGTTGGTCCGCTACTGAGTGACACAAAGTGAATAC 70

Oy 981 aacacacgttggtcgctctccaaagctgtcagaagtgatccttggtcccaagacagctcg 1040
Db 71 AACCAACTGTGGCCGCTCTCCACAGCTGCTCAGAGTGATCTCGGCCCAAGACCACTCTG 130

Oy 1041 tgcctggagctccggtgagtgagtggtgtggtcccaatgctgagcagcagaggttggc 1100
Db 131 TGCCCTGGAGCTTCGGGCTGGATGATGTGTGGCCCATGCGGGGAGACCGAGGGTTGGT 190

Oy 1101 ccaagacatagatcagacagatgtctcctcttctgttccctaaagagccttgagaaactgc 1160
Db 191 CCAAGACATAGATCAGACAGATGTCTCCTCTTGTGTCTTAAGAGCCTGGAGAAAGCTGC 250

Oy 1161 agtagtggttgaagttcccggtgtgtacagctgagcagtggtgtgtgtgtgtgtgtgt 1220
Db 251 AGTAGTGTTTGAAGTTCCCGTGTGGCTACACCTTCGCATGTGTGTGTGTGTGTGTGTGT 310

Oy 1221 ctacagcatgagcagctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1280
Db 311 CTCACATGAGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 370

Oy 1281 gcgggagctgagctgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1340
Db 371 GCGGATGAGACTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 430

Oy 1341 tcaggaaggttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1400
Db 431 TCAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 490

Oy 1401 agatgtctcgaagcggcgccacacacagtgagggcgagagctgtgtgtgtgtgtgtgtgt 1460
Db 491 AGATGCTCGAGCGCGGGCCACACAGTGGGGGAGCTGTGTGTGTGTGTGTGTGTGTGTGT 550

Oy 1461 tctcgagcatcctctgtactctatctctgattgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1520
Db 551 TCTCGACATCCTCTGACTCTCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 610

Oy 1521 ggaactctgtgttagaagaagaagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1580
Db 611 GGAATCTTGCTTANAGCAAGTGCGCTGTGACCTGTGGGGCTTCACCTTCTGTGGAGCAC 670

Oy 1581 aagctacagcagaagcct 1599
Db 671 AAGCTACAGCAAGACCT 689

RESULT 3
LOCUS AI379133 459 bp mRNA EST 18-MAR-1999
DEFINITION t659g09.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2068960
ACCESSION AI379133
VERSION AI379133.1 GI:4188986
KEYWORDS EST.
SOURCE human.
```

```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 459)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1306 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 439.

FEATURES
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1..459
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone.lib="MAGE:2068960"
/clone.lib="Soares_NHMPu_S1"
/tissue.type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab.host="DH10B"
/Note="Organ: mixed (see below); Vector: p773D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbH, pregnant uterus
2NbH, and fetal heart 2NbH19H) were mixed, and 98 clones
were used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT      142 a      117 c      105 g      95 t
ORIGIN

Query Match      19.4%; Score 449; DB 19; Length 459;
Best Local Similarity 100.0%; Pred. No. 9.2e-231;
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1867 tctcttgagatgagtgatctactgtgattttagatctgtctctctgtgagctgtgattg 1926
Db 459 TCTCTTGTAGATGAGTGAATCTTGATTTAGATCTGTCTCTGTGAGCTGTGATGG 400

Oy 1927 gcttggtggcagaacctgtgctgtgattccatgagagaatcagaagctgttctctg 1986
Db 399 GCTTGGGGCCAGACCTTGGCTGTGATTCCTGATTCAGAAATCAGAAATGCTTTTCTG 340

Oy 1987 cagcaaatcagagcttcccccatacatctgaactcctgttaaccttaccctgtgcccc 2046
Db 339 CAGCAAAATCAGAGGCTTCCCTTAACATCTGAATCTCTGTAACCTTTCATCCTGTGCCCC 280

Oy 2047 tatcttggtgcccattagtttggtgagtgagggcacagggcatagctatgactgttctt 2106
Db 279 TATCTTGGGGCCCATAGTATTGGGATGGGACAGGGCATGTGATGACTTTGCTTTCT 220

Oy 2107 ggttgagccttggtgggaaagaagccctgtgagtggtgtgtgtgtgtgtgtgtgtgtgt 2166
Db 219 GGTGTGAGCCTGTGGCGGAAGAAGCCCTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGT 160

Oy 2167 tctctggagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2226
Db 159 TCCTTGGGGTGTGTCTCTTATTTCTTCAAGTTTATCTGATGTGTGGGAGTGATGATC 100

Oy 2227 cccatgttgcaatatagagctctgtccctgagatcttcccatcctcaagtttctctcat 2286
Db 99 CCCATGTTCATATGAGATCTCTGCCCTGAGATCTTCCCATCTCCCATCTTCAGTTTCTTCCAT 40

Oy 2287 gaagagtagctgttaataacatagtgctc 2315
```

```
Db 39 GAAAGACTAGCTGAATACATAGTCTTC 11
|||||
RESULT 4
LOCUS AI942370 456 bp mRNA EST 08-MAR-2000
DEFINITION WO80E06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:246166 3',
ACCESSION AI942370
VERSION AI942370.1 GI:5707026
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 456)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 760 Std Error: 0.00
Seq primer: -40UP from Glbco
High quality sequence stop: 405.
FEATURES
source
1. 456
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="IMAGE:246166"
/clone_1ib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid11 was
prepared, and as circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
```

```
BASE COUNT 142 a 116 c 105 g 93 t
ORIGIN
Query Match 17.3%: Score 401; DB 104; Length 456;
Best local similarity 99.8%: Pred. No. 7.7e-205;
Matches 451; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1864 agtctctttagatagatgactttagatttagatctgtctctcgtgagctgga 1923
|||||
Db 456 AGTCTCTTGTGATATAGATGATTACTTGATTTAGTATCTGTCTCTGAGCCCTGA 397
QY 1924 tgggtctggggccaagacttgcctgattcccatgagaaatcagaactgctt 1993
|||||
Db 396 TGGGCTTGGGGCCAGACCTTGGCTGATTCCTCATTCAGAAATCAGAACTGCTTT 337
QY 1984 ctgcagcaaatcagagcttcccccataactcgaactccgtaactcattccctggcc 2043
|||||
Db 336 CTGACAGCAATTCAGGCTTCCCTTACATCTGAACTCTGTAAACCTTCATCCCTGGCC 277
QY 2044 ccctattctggcccatgatttgggattgggacagagcagatagctgacttgctt 2103
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Db 276 CCTATCTTGGGCCCATTTAGTTGGGATGGGACAGGCGCATAGCTATGACTTCTT 217
|||||
QY 2104 tctggttggagccctggcgggaagagccctggagtggttggggcaaatgctgccc 2163
|||||
Db 216 TCTGCTTGGAGAGCTTGGCCGGAAGAGAGCCCTGAGAGTGTTGGGGCAAACTGCCCCT 157
QY 2164 gactcctgggggtgctctctcttcttctcgaattctcgaatctgtggggaatgcatg 2223
|||||
Db 156 GAGTCCTTGGGGTGGTCTCTGCTTATTTCTCAAGTTATCTGAAATCTTGGGGAGTGCATG 97
QY 2224 atcccattgtgaatctgagctctgcctcgagatcttcacatcgaattctctc 2283
|||||
Db 96 ATCCCATGTTGCAATATGCAATCTCTGCCCTGAGATCTTCCCATCTCATTTCCCTTC 37
QY 2284 catgaagagtaagtgtaataacatagtgctc 2315
|||||
Db 36 CATGAAGAGTACCTGTAAATACATAGTCTTC 5
```

```
RESULT 5
LOCUS AA459837 503 bp mRNA EST 09-JUN-1997
DEFINITION 2x30g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795718
ACCESSION AA459837
VERSION AA459837.1 GI:2184744
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Giesel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,
T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 459.
FEATURES
source
1. 503
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:6039163"
/db_xref="taxon:9606"
/clone_1ib="IMAGE:795718"
/clone_1ib="Soares_testis_NHT"
/lab_host="DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - Oligo(dT) primer [5',
TGTTACCAATCTGAGAGGAGGCGGCCCAATTTTGTGTTTGTGTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

```
BASE COUNT 105 a 136 c 149 g 113 t
ORIGIN
Query Match 16.2%: Score 375; DB 7; Length 503;
```


source

```
1. .407
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="1877444"
/clone_lib="Scars_NbHh19w_S1"
/tissue_type="pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below): Vector: p7773D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHh, pregnant uterus
NbHhPU, and fetal heart NbHh19w) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484408-489479."
```

BASE COUNT

118 a 106 c 96 g 87 t

Query Match	14.0%	Score 325	DB 18	Length 407
Best Local Similarity	100.0%	Pred. No.	8.5e-164	
Matches 325	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1591	aaatcaagagctccccctaaacacatgaactccctgtaaaccttcacccctggcccctac	2050
Db	335	AAATCAGAGGCTCCCTCATCTGACTGACTCCGTAAACCTTCATCCCTGGCCCCCTATC	276
Qy	2051	ttgggcccattagtttttggggaatggggcaagggacatgacttgacttgctttcagtc	2110
Db	275	TTGGGGCCCATATGATTTTGGGATGGGGCACAAGGCCATACCTATGACCTTTGGCTTGCTT	216
Qy	2111	ggaagccctggccggaagaaagaagccctcgaggagtagtggggggcaaatgtgccttagtctc	2170
Db	215	GGAGCCTGGCCGGAGAGAGAGCCCTGGAGGTGGTTGGGGCGAATGTGGCCTAGTACT	156
Qy	2171	ttggggtgtcttcgtctatcttttcaagtcttacttgaaatctgtgggagtgcatgatcccca	2230
Db	155	TGGGGTGTTCTCGTATATTTCTTAAATTTTATCTGAAATCTGTGGGAGATGATATCCCA	96
Qy	2231	tgatgcgaataatggagctctcgcccctbagaatcctcccatctcaagcttctccatccataaa	2290
Db	95	TGTTGCATATATGAGTCCTGCCCCGATGATCTCCCATCTCAGTTTCTTCATGAAA	36
Qy	2291	gaagtaagtgtaaatatcatagttctc	2315
Db	35	GAGTACGTGTAAATACATATATGTCTC	11

LOCUS	H24181	437 bp	mRNA	EST	06-JUL-1995
DEFINITION	YB55F02.1 Soares infant brain JMB Homo sapiens cDNA clone IMAGE:52280 5' similar to SP:A49069 A49069 COLLA2P1IN - , mRNA sequence.				
ACCESSION	H24181				
VERSION	H24181.1	GI:892876			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 437)				
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., R., Williamson,A., Wohldmann,P. and Wilson,R.				
TITLE	The Mashu-Merck EST Project				
JOURNAL	Unpublished (1995)				
COMMENT	Contact: Wilson RK				

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 1989
High quality sequence stops: 310 Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1989 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 310.

FEATURES	Location/Qualifiers
source	1. .437

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/organism="Homo sapiens"
/db_xref="db:425216"
/db_xref="taxon:9606"
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/clone_1lb="Soares Infant brain INTB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: latmid BA; Site: 1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGGCGCCGACGAAATTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the latmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo."

```

Query Match	12.9%	Score 298;	DB 153;	Length 437;
Best Local Similarity	100.0%	Pred. NO. 3.3e-149;		
Matches 298; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	488	gaccacaagacatctggagcaatgacgaatgtgtccctcaagaagataaacaatgacga	547
Db	1	GACCACAAAGACATTGGACAGAGTCGATGGTCCCTTGAGAGAACTAAACATAGACTGCA	60
OY	548	acagaagacatgcctctgctgtagcaaatgtaatgtgtcccaagaccagacatgtagatgacatca	607
Db	61	ACAGAGGACATGCTCTGTGGACAAATGATGTGCCCAACCCAGACCTTGAGAGATGCAATCA	120
OY	608	ccaacaacatgaagatctcgagcaacttggactatctctctctcctgctgaacggatracca	667
Db	121	CCACACAAATGATAGTCCGGCACTTTGGCTATCTCTCTCCCTGCTTACCGCGTACTCA	180
OY	668	ccctcatccggagaccacccactcatctggaacagagcagatgttccagctgaatgacacccc	727
Db	181	CCTTCATCCGGGACCAACCCACTCATGAGACAGGCCAGTGTTCACACTGATGGGCCACCCCC	240
OY	728	tgtctgttcaactaagatatcagactatcttcacagatgtgtgtgccaagaggttgacacgct	785
Db	241	TGCTGTGTCACTACACATACAGCTATCTTCAGAGTGTGTGCCACACAGGGTGACCAACCTT	298

RESULT	9
LOCUS	BE734978
DEFINITION	BE734978 1045 bp mRNA EST 15-SEP-2000 601570573F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:3844914 5', mRNA sequence.
ACCESSION	BE734978
VERSION	BE734978.1 GI:10149073
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. (bases 1 to 1045)
REFERENCE	1


```

RESULT 11
LOCUS 245329 337 bp mRNA EST 14-NOV-1994
DEFINITION HSCM091 normalized infant brain cDNA Homo sapiens cDNA clone
ACCESSION c-2mg09, mRNA sequence.
VERSION 245329
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 337)
Auffray,C., Behar,G., Bols,F., Bouchier,C., da Silva,C., Devignes
,M.D., Duprat,S., Houllatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F.,
Mitchell,H., Marlage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabakchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
JOURNAL 95277534
MEDLINE
COMMENT Contact: Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 Evry Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_id: C; Genexpress_sequence_id: y1c-2mg09
Seq primer: (-21)M13-universal.
FEATURES
source
1. 337
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-2mg09"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain
total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
BASE COUNT 81 a 106 c 82 g 67 t 1 others
ORIGIN
Query Match 10.2%; Score 235; DB 159; Length 337;
Best Local Similarity 99.4%; Pred. No. 3.4e-115;
Matches 335; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 487 caccaccaagacatcggagcagtcgaaatggtcccttcagaaactaaacatgctgc 546
|||||
DB 1 CGACCAAGACATTCGGACAGTGTGAATGGTCCTTCAGAGACTAAACATGACTGC 60
QY 547 aacagagagctgctgtcgtgagacaaatgltgcccagaccagactggagagtgatc 606
|||||
DB 61 AACAGAGGAGCTGCTGTNGTGACATGATGTGCCAGGCCAGACTGAGAGTGATC 120
QY 607 accaacaacatgaagctccggacattgtgcatctctctccctgctgacgcgtactc 666
|||||
DB 121 ACCAACAATGATGAAGCTCGGCACTTGGCTCATCTCTCCCTGCTGACCGCTACTC 180
QY 667 accttcatcggagaccaccaactcagagcagagtgcttccacatgtagccacccc 726
|||||
DB 181 ACCTTATCCGGAGACCAACCACTCATGATGACAGCCAGTGTTCACAGTGCACACCCC 240

```

```

QY 727 ctgctgtcactacacagatatactcagagtcgtgcccacaggtgacgctc 786
|||||
DB 241 CTGCTGTACTACTACAGTTACAGGCTATCTCAGAGTGTGGCCACAGAGGTGACAGCTC 300
QY 787 tcagagaaagatatagtatgtctctactctggagacg 823
|||||
DB 301 TCAGGGAACACTATGATGTCTCTACTCTGGGACAG 337
RESULT 12
LOCUS A0352219 592 bp DNA GSS 24-JAN-1999
DEFINITION CITR1-El-2536H11.TF CITR1-El Homo sapiens genomic clone 2536H11,
DNA sequence.
ACCESSION A0352219
VERSION A0352219.1 GI:4179554
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 592)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
JOURNAL Other_GSSs: CITR1-El-2536H11.TF
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeet@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
FEATURES
source
1. 592
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2536H11"
/clone_lib="CITR1-El"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 140 a 171 c 143 g 136 t 2 others
ORIGIN
Query Match 9.4%; Score 218; DB 205; Length 592;
Best Local Similarity 100.0%; Pred. No. 5.4e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 599 agtgcattaccacaacaatgaagctccggacattgtgcatatctctccctgac 658
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DB 270 AGTGCATCAACAACAACATGAAGCTCCGGCAGCTTGGCTCATCTCTCCCTGAC 329
QY 659 gggctactcaacttcaatccggagaccacacatcagagcagagtggttccagctgatg 718
|||||
DB 330 GCGTACTCACCTTCATCCGGGACCCACCACTCATGACAGCCAGTGTTCAGCTGATG 389
QY 719 gccacccctctgctgcatcacagatatacagcctatctcagagtcgtgcccacaggtga 778
|||||
DB 390 GCCACCCCTGCTGCTGACATGATGATGACAGATGATGATGATGATGATGATGATGATG 449
QY 779 ccagctctcaggaagagatgatgtgctctactctg 816
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```

DB	450	CCAGCCTCTCACGGAAGAAGATATGATGTCTTACTCGT	487
RESULT	13		
LOCUS	T09073	364 bp	mRNA
DEFINITION	EST06966 Infant Brain, Bento Soares Homo sapiens		CDNA clone HIBB071
ACCESSION	T09073		
VERSION	T09073.1	GI:390101	
KEYWORDS	5' end mRNA sequence.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.		
JOURNAL	Rapid CDNA sequencing (expressed sequence tags) from a		
MEDLINE	directionally cloned human infant brain cDNA library		
COMMENT	Nature Genet. 4, 373-380 (1993)		
FEATURES	94004965		
source	Contact: Adams, MD The Institute for Genomic Research 932 Clopper Road, Gaithersburg, MD 20878 Tel: 3016699056 Fax: 3018699423 Email: mdadams@tigr.org Seq primer: M13 Reverse. Location/Qualifiers 1..364 /organism="Homo sapiens" /db_xref="ATCC (inhost):85555" /db_xref="taxon:9606" /clone="HIBB071" /clone_lib="Infant Brain, Bento Soares"		
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ORIGIN			
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Best Local Similarity	99.6%; Pred. No. 1.8e-105;		
Matches	267; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
OY	922 aaatgtacacagctgctccctggcttgctcgcgtactaggtagcacaaagtatatca	981	
Db	1 AATGTGTACCACAGCTGGCTCCTGGTTGGTCGCCCTACTGAGTGACACAAGTAATCA	60	
OY	982 accaacctgtgcccgtcttcacagagctcgcttcagagtgcattccctggccccagaaccagttcgt	1041	
Db	61 ACNAACTGTGGCGGCTCTCCACAGCTGCATCAGAGTGCATCTCGCCCCACACCACTGTCT	120	
OY	1042 gccctgagacctccagctgtaglaagatgttgtgcccacatgccag999agcacaggaagttgttc	1101	
Db	121 GCCCTGACACTTCGCCGCTCGATGACGTGTGTGGCCCATGCCGGGAGACACCGAGGTGGTC	180	
OY	1102 caagacatagagctcagcagatgtctcctcttcttgcttaagagcctcygagaaagtcca	1161	
Db	181 CAAGACATAGAGTCAAGCATAGTGTCTCTTGTGTCTTAAGAGCTGAGAACGTCCA	240	
OY	1162 gtatggtttgaagttcccgctggtctacag	1189	
Db	241 GTAGTGTTTGAAGTTCCCGCTGCTACAG	268	
RESULT	14		
LOCUS	H10410	413 bp	mRNA
DEFINITION	yhb8907.g1 Soares Infant brain INIB Homo sapiens		CDNA clone
ACCESSION	H10410		
VERSION	H10410.1	GI:875232	
KEYWORDS	EST.		
SOURCE	human.		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
ORGANISM	Homo sapiens	Human		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P., Treviski, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.			
TITLE	The Washu-Merck EST Project			
JOURNAL	Unpublished (1995)			
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu Insert Size: 1985 High quality sequence stops: 307 Source: IMAGE Consortium, LNLN This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert length: 1985 Std Error: 0.00 Seq primer: Promega -2lm13 High quality sequence stop: 307. Location/Qualifiers 1. .413 /organism="Homo sapiens" /db_xref="GDB:419839" /db_xref="taxon:9606" /clone="IMAGE:47298" /clone_lib="Soares Infant brain INIB" /sex="female" /dev_stage="73 days post natal" /lab_host="DH10B (ampicillin resistant)" /note="Organ: whole brain; Vector: Lambda BA; Site:1: Not I; Site:2: Hind III; 1st strand cDNA was primed with a NOT I - oligo(dT) primer [5' AACTGAGAATTTGCGCCGACGAGAAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lambda BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Patima Bonaldo."			
FEATURES	Source			
BASE COUNT	112 a 100 c 102 g 94 t 5 others			
ORIGIN				
Query Match	9.1%; Score 211; DB 152; Length 413;			
Best Local Similarity	100.0%; Pred. No. 3.1e-102; Indels 0; Gaps 0;			
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 2105	ctggttcgagccctgagcgaagaagagccctgagtggtgtcgtgagcgaatgtgcctg 2164			
Db 227	CTGGTTCGAGCCCTGCGCCGGAAGAAGAGACCCCTGAGGTGTGTTGGGGCAATGTCCCTG 168			
QY 2165	agctcttgagggtgtgtctgcgtattctctcaagttatctgaatctctgtggagagtcarga 2224			
Db 167	AGTCTCTTGGGGGTGCTGCTTATTCCTCAAGTTATTCGATCTGTGGGGAGTGCATGA 108			
QY 2225	tcgccatttcgaatatagatctctgcgccctgagatctcccatctagtttctctcc 2284			
Db 107	TCCCATCTTTCGAATATGAGAGTCTGTCCCGAGATCTTCCCATCTCAGTTTTCCTTCC 48			
QY 2285	atgaaagagtcagtgtaatacatagtgctc 2315			
Db 47	ATGAAGAGTACGTGTAAATACATAGTCTTC 17			
RESULT 15	AA937917 317 bp mRNA EST 24-AUG-1998			
LOCUS	AA937917/c			
DEFINITION	of72e01.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1435896 3', mRNA sequence.			

ACCESSION AA937917
VERSION AA937917.1 GI:3096028
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 317)
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA library preparation: M. Bento Soares, Ph.D.

CDNA library arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 1661 Std Error: 0.00

Seq. Primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 315.

Location/Qualifiers

FEATURES

source

1..317

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_1lib="NCI-CGAP_C08"

/issue_type="adenocarcinoma"

/lab_host="DH10B"

/note="Organ: colon. Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker. 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaudo."

BASE COUNT 97 a 82 c 77 g 61 t

ORIGIN

Query Match 8.4%; Score 195; DB 14; Length 317;

Best Local Similarity 99.7%; Pred. No. 1.3e-93;

Matches 315; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 317 CTCCCCCTACATCTGAACCTCTGTAAACCTCATCCCTGCCCCCTATCTGGGCCA 258
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OY 2060 ctatgttctgggagctgggacagggacatgacatcttctctgttggagccttg 2119
|||||
DB 257 TTAGTTTGGGAGTGGGGCACAAGGCATACCTTGTCTTCTGTTGGAGCCTGG 198
|||||
OY 2120 cgggaaggaagacccctggaggtggttggggggaatgctgacctgagctctgggtgtg 2179
|||||
DB 197 CCGGAAGGAAGACCCCTGAGGTGCTT-GGGGCAAAATGCTCCTGACTCCTTGGGGTGT 139
|||||
OY 2180 tctgctatctctcaagttatctgaatctgltggggagtgacgacaloccccatgttgcac 2239
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DB 138 TCTGCTATTCTCTCAAGTTATCTGAATCTGTGGGAGTGCATGATCCCATGTGCAAT 79
|||||
OY 2240 atggagctctgcctcgagatcttcccatctagtttcttccatgaaagagtagctg 2299
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DB 78 ATGAGTCTCTGCTGAGATCTTCCCATCTAGTTTCTTCATGAAGAAGTACGTG 19
|||||
OY 2300 taaatcatagtttc 2315
|||||
DB 18 TAAATACATAGTCTTC 3

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